RAW SEQUENCE LISTING
ERROR REPORT
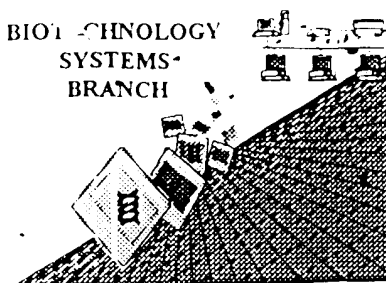
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09 614 221_

Source: _OIPE_

Date Processed by STIC: _11/16/01_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW.

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/614 221

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY P

1 _____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .5; this will prevent "wrapping."

2 _____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length.

Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If Intentional, please insert the following lines for each skipped sequen
<210> sequence id number
<400> sequence id number
000

9 ✓ _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

10 _____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species) <220>-<223> section is required when <213> response is Unknown is Artificial Sequence

11 _____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 . _____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represe any value not specifically a nucleotide.

AMC/MII – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 11/16/2001
PATENT APPLICATION: US/09/614,221   TIME: 10:41:23

Input Set : N:\jumbos\614221.raw
Output Set: N:\CRF3\11162001\I614221.raw

```
 2 <110> APPLICANT: Karunanandaa, Balasulojini
 3        Yu, Jaehyuk
 4        Kishore, Ganesh M.
 6 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
 7        WITH STEROL SYNTHESIS AND METABOLISM
 9 <130> FILE REFERENCE: 05686.0004.NPUS00
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/614,221
C--> 11 <141> CURRENT FILING DATE: 2000-07-11
11 <150> PRIOR APPLICATION NUMBER: US 60/142,981
12 <151> PRIOR FILING DATE: 1999-07-12
14 <160> NUMBER OF SEQ ID NOS: 626
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1358
18 <212> TYPE: DNA
19 <213> ORGANISM: Glycine max
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (24)...(1100)
25 <400> SEQUENCE: 1
27 gaattcggct cgagtttgaa cca atg aca atg ctt cag aaa atg gct gag ctt      53
28                         Met Thr Met Leu Gln Lys Met Ala Glu Leu
29                          1               5                  10
31 atg gag tac tct tac ctg tta gat atg gcg gac aag act gag gat cca     101
32 Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro
33              15                  20                  25
35 tac atg aga cta gta tat gct tca tca ttc ttt ata tct gtc tac tat     149
36 Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr
37              30                  35                  40
39 gcc tat caa cga acg tgg aag cca ttc aat cca att ctt ggt gag act     197
40 Ala Tyr Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr
41              45                  50                  55
43 tat gaa atg gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc     245
44 Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val
45       60                  65                  70
47 agt cat cac cct cca atg agt gct ggg cat gct gaa act gaa cat ttc     293
48 Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe
49 75                  80                  85                  90
51 act tat gat gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca     341
52 Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser
53              95                 100                 105
55 gtt gat gta tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat     389
56 Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp
57             110                 115                 120
59 ggt gtg gtc ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg     437
60 Gly Val Val Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu
61             125                 130                 135
63 att ttt gga cga act tgg att gat tca cca gga gag atg atc ctg aca     485
```

Errored
Must enumerate unknowns
See sample page 5 of 8

RAW SEQUENCE LISTING   DATE: 11/16/2001
PATENT APPLICATION: US/09/614,221   TIME: 10:41:23

Input Set : N:\jumbos\614221.raw
Output Set: N:\CRF3\11162001\I614221.raw

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64 Ile Phe Gly Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr
65     140                 145                 150
67 aat ctg act aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc       533
68 Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly
69 155                 160                 165                 170
71 tgg ttt gga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag       581
72 Trp Phe Gly Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu
73                 175                 180                 185
75 cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa       629
76 Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln
77             190                 195                 200
79 gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag       677
80 Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
81         205                 210                 215
83 att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg       725
84 Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr
85     220                 225                 230
87 cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg       773
88 His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
89 235                 240                 245                 250
91 ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag       821
92 Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys
93                 255                 260                 265
95 ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg       869
96 Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg
97                 270                 275                 280
99 caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act       917
100 Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr
101             285                 290                 295
103 cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt      965
104 Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly
105     300                 305                 310
107 gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct      1013
108 Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala
109 315                 320                 325                 330
111 gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa      1061
112 Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu
113                 335                 340                 345
115 ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcatcct      1110
116 Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu
117             350                 355
119 tgtggaattc tttctatttt ttttaaatat catttgtta ttaagtttgt aatgtaatct    1170
121 tgattggaat gcttgaaatt tggttttgtt tttgggttgt tttatcactg tagtatttga    1230
123 ttaattaata gtagctatgt tagttcatca gttcactttg catggataaa tgctagtagg    1290
125 gaaattaaag ttatcttcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaagggc      1350
127 ggccgccg                                                              1358
130 <210> SEQ ID NO: 2
131 <211> LENGTH: 1136
132 <212> TYPE: DNA
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RAW SEQUENCE LISTING   DATE: 11/16/2001
PATENT APPLICATION: US/09/614,221   TIME: 10:41:23

Input Set : N:\jumbos\614221.raw
Output Set: N:\CRF3\11162001\I614221.raw

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133 <213> ORGANISM: Glycine max
135 <220> FEATURE:
136 <221> NAME/KEY: CDS
137 <222> LOCATION: (73)...(975)
139 <400> SEQUENCE: 2
141 gaattcggct cgaggtcaca acttcagtgc tatggtgaat cagtgtattg cacaggttcg      60
143 gacttgctaa gc atg tgc aac aat ggt cag agt cca ctt gat agg ttc ata     111
144              Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile
145               1                   5                  10
147 tct gtg gta gca tgg tgc ata tct acc act cgc cct gtg act ttt ggt      159
148 Ser Val Val Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly
149     15                  20                  25
151 gtt gct cct tat aat ccc att ctt ggt gag aca cac cat gtt tca agg      207
152 Val Ala Pro Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg
153 30                  35                  40                  45
155 gga aat ctt aat gtg tta ttg gag cag att tca cat cac cct cca gta      255
156 Gly Asn Leu Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val
157                 50                  55                  60
159 act gct ctc cat gca aca gat gag aag gaa aac att gaa atg tta tgg      303
160 Thr Ala Leu His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp
161             65                  70                  75
163 tgc cag cga cct gat cca aag ttt aat ggc aca tca gtt gaa gct aaa      351
164 Cys Gln Arg Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys
165         80                  85                  90
167 gtg cat gga ata cgc cag ttg aag ctc cta aat cat ggt gaa aca tat      399
168 Val His Gly Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr
169     95                  100                 105
171 gaa atg aat tgt cct cgc ctt tta ctt aga att ctt cca gtt cct ggt      447
172 Glu Met Asn Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly
173 110                 115                 120                 125
175 gct gat tgg gct ggt aca gtt aat ata cgg tgc cta gag aca ggt cta      495
176 Ala Asp Trp Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu
177             130                 135                 140
179 gta gct gaa tta tcc tac aga tca agt tct ttt cta gga att ggg ggg      543
180 Val Ala Glu Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly
181             145                 150                 155
183 aat cat aga gtg atc aaa ggg aag atc ctt gac tct tca tca ttg aaa      591
184 Asn His Arg Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys
185             160                 165                 170
187 gtt cta tat gaa gtt gat ggt cat tgg gat agg acc gta aaa gtg aag      639
188 Val Leu Tyr Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys
189     175                 180                 185
191 gac aca aat aat ggg aaa gta aga gtg ata tat gat gca aag gaa gtt      687
192 Asp Thr Asn Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val
193 190                 195                 200                 205
195 atg tca ggt ctc gaa act cct ata ctc aag gac ata gag ggt gtg tgg      735
196 Met Ser Gly Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp
197             210                 215                 220
199 caa aca gaa tca gct cat gtt tgg ggt gaa tta aac caa gcc att gtg      783
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/614,221

DATE: 11/16/2001
TIME: 10:41:23

Input Set : N:\jumbos\614221.raw
Output Set: N:\CRF3\11162001\I614221.raw

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200 Gln Thr Glu Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val
201             225             230             235
203 agc aaa gac tgg gag aaa gca aga gaa gca aag cta aaa gtt gag gaa      831
204 Ser Lys Asp Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu
205             240             245             250
207 aga caa agg gag ctt gtg aga gaa aga gaa tca aaa gga gaa aca tgg      879
208 Arg Gln Arg Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp
209     255             260             265
211 att tct aag cat ttt gta gtt tct aac aac aaa gaa ggg tgg caa tgt      927
212 Ile Ser Lys His Phe Val Val Ser Asn Asn Lys Glu Gly Trp Gln Cys
213 270             275             280             285
215 tca cct att cat aag agt gta cct gcg gcc ccc atc aca gcc cta taa      975
216 Ser Pro Ile His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu
217             290             295             300
219 ttgttgtcac tgtcaagtag tgtaaagcat taaagtacat tttagaagag aatgttcata   1035
221 aaaaaattta atggttgaaa ttttgacaac aatgaagtat ataacaaaat ttaaaattag   1095
223 ttacaatttt aaaaaaaaaa aaaaaaaaag ggcggccgcc g                       1136
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 1355
228 <212> TYPE: DNA
229 <213> ORGANISM: Glycine max
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (32)...(1099)
235 <400> SEQUENCE: 3
237 ggaattcggc tcgaggacaa tgcttcagaa a atg gct gag ctt atg gag tac        52
238                                   Met Ala Glu Leu Met Glu Tyr
239                                   1               5
241 tct tac ctg tta gat atg gcg gac aag act gag gat cca tac atg aga      100
242 Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg
243         10              15              20
245 cta gta tat gct tca tca ttc ttt ata tct gtc tac tat gcc tat caa      148
246 Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln
247     25              30              35
249 cga acg tgg aag cca ttc aat cca att ctt ggt gag act tat gaa atg      196
250 Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met
251 40              45              50              55
253 gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc agt cat cac      244
254 Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His
255             60              65              70
257 cct cca atg agt gct ggg cat gct gaa act gaa cat ttc act tat gat      292
258 Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp
259             75              80              85
261 gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca gtt gat gta      340
262 Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val
263             90              95              100
265 tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat ggt gtg gtc      388
266 Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val
267     105             110             115
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RAW SEQUENCE LISTING   DATE: 11/16/2001
PATENT APPLICATION: US/09/614,221   TIME: 10:41:23

Input Set : N:\jumbos\614221.raw
Output Set: N:\CRF3\11162001\I614221.raw

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269 ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg att ttt gga    436
270 Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly
271 120                 125             130                 135
273 cga act tgg att gat tca cca gga gag atg atc ctg aca aat ctg act    484
274 Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr
275                 140             145                 150
277 aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc tgg ttt gga    532
278 Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly
279                 155             160                 165
281 gct ggt aga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag    580
282 Ala Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu
283                 170             175                 180
285 cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa    628
286 Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln
287         185             190             195
289 gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag    676
290 Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
291 200                 205             210                 215
293 att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg    724
294 Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr
295                 220             225                 230
297 cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg    772
298 His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
299                 235             240             245
301 ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag·   820
302 Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys
303         250             255             260
305 ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg    868
306 Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg
307         265             270             275
309 caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act    916
310 Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr
311 280                 285             290                 295
313 cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt    964
314 Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly
315                 300             305                 310
317 gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct   1012
318 Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala
319                 315             320             325
321 gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa   1060
322 Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu
323         330             335             340
325 ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcatcct   1109
326 Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu
327         345             350             355
329 tgtggaattc tttctatttt tttgaaatat cattttgtta ttaagtttgt aatgtaatct 1169
331 tgattggaat gcttgaaatt tggtttttgtt tttgggttgt tttatcactg tagtatttga 1229
333 ttaattaata gtagctatgt tagttcatca gttcactttg catggataaa tgctagtaga 1289
335 gaaattaaag ttaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaagggcgg 1349
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VERIFICATION SUMMARY　　　　　　　DATE: 11/16/2001
PATENT APPLICATION:　**US/09/614,221**　　TIME: 10:41:24

Input Set : **N:\jumbos\614221.raw**
Output Set: **N:\CRF3\11162001\I614221.raw**

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L:11  M:270 C: Current Application Number differs, Replaced Current Application No
L:11  M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:644 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:644 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:646 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:646 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:648 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:648 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:661 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:661 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:661 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:663 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:663 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:663 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:665 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:665 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:667 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:667 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:718 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:11
L:718 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:11
L:718 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:757 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:757 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:763 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:13
L:763 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:778 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:778 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:778 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:788 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:14
L:788 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:809 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:15
L:809 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:15
L:809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:844 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:844 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:846 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:846 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:923 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
```

VERIFICATION SUMMARY   DATE: 11/16/2001
PATENT APPLICATION: **US/09/614,221**   TIME: 10:41:24

Input Set : **N:\jumbos\614221.raw**
Output Set: **N:\CRF3\11162001\I614221.raw**

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L:923  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:923  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:992  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:992  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:992  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:994  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:994  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:994  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:996  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:996  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:996  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:998  M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:24
L:998  M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24
L:998  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1013 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1013 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1013 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1015 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1015 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1015 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1017 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1017 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1017 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1019 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
L:1019 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
L:1019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1032 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
L:1032 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
L:1032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1057 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1061 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1063 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1065 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1067 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1088 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1090 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1092 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1094 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1096 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1109 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1111 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
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